

Figure 1

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1 2 3 4 5 6 7 8 9 10 11 12 13

A

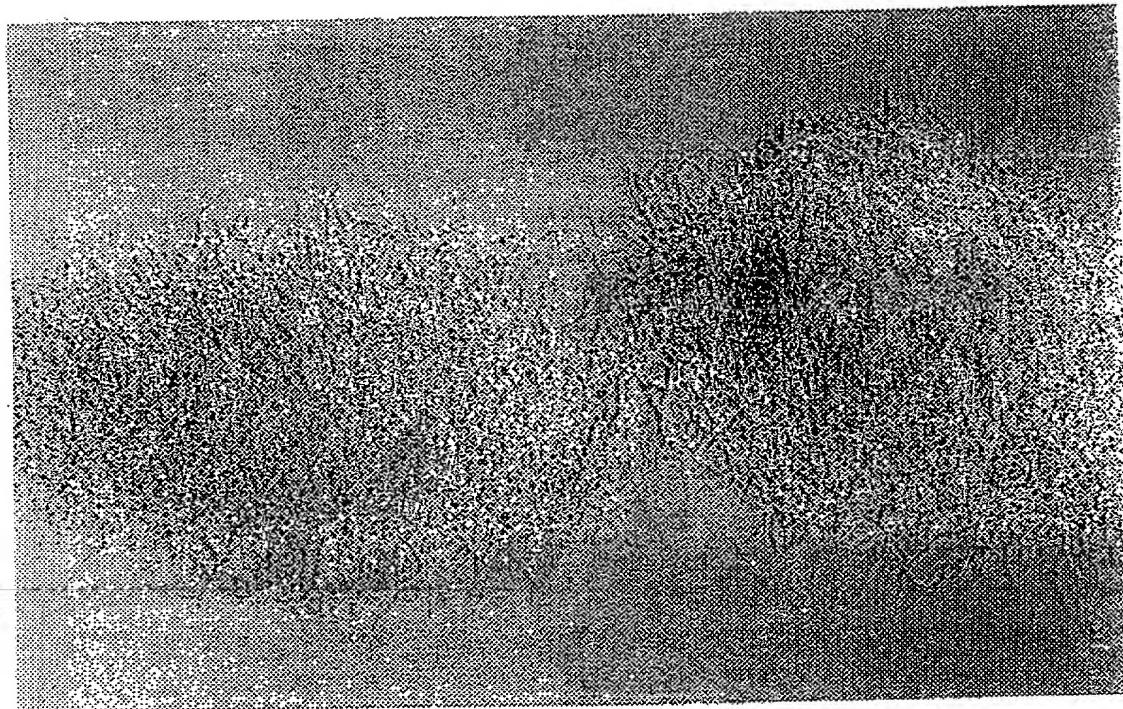


1 2 3 4 5 6 7 8 9 10

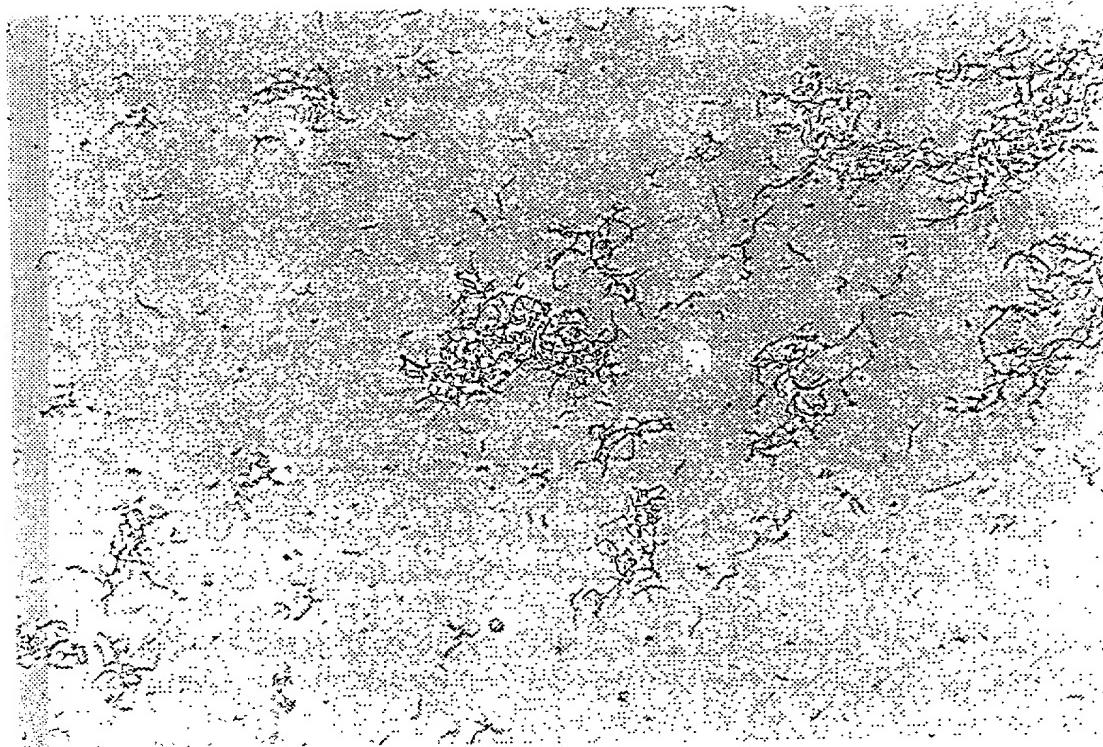
B



Figure 2



A



B

Figure 3

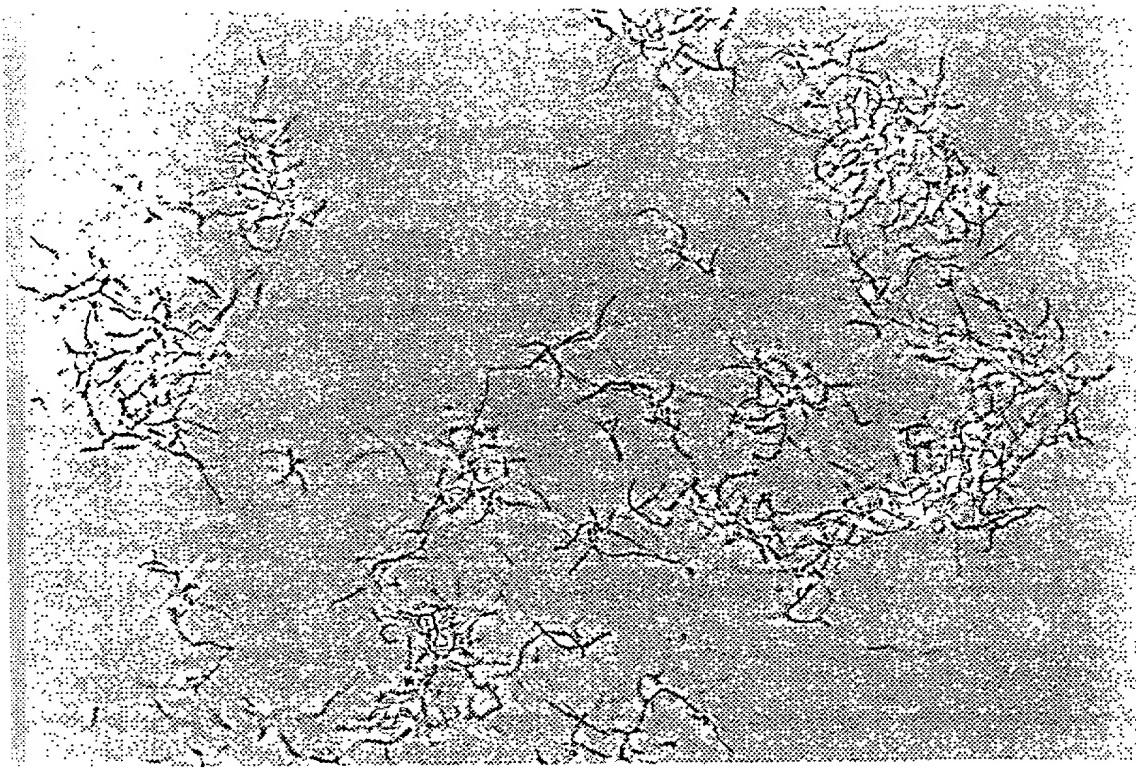
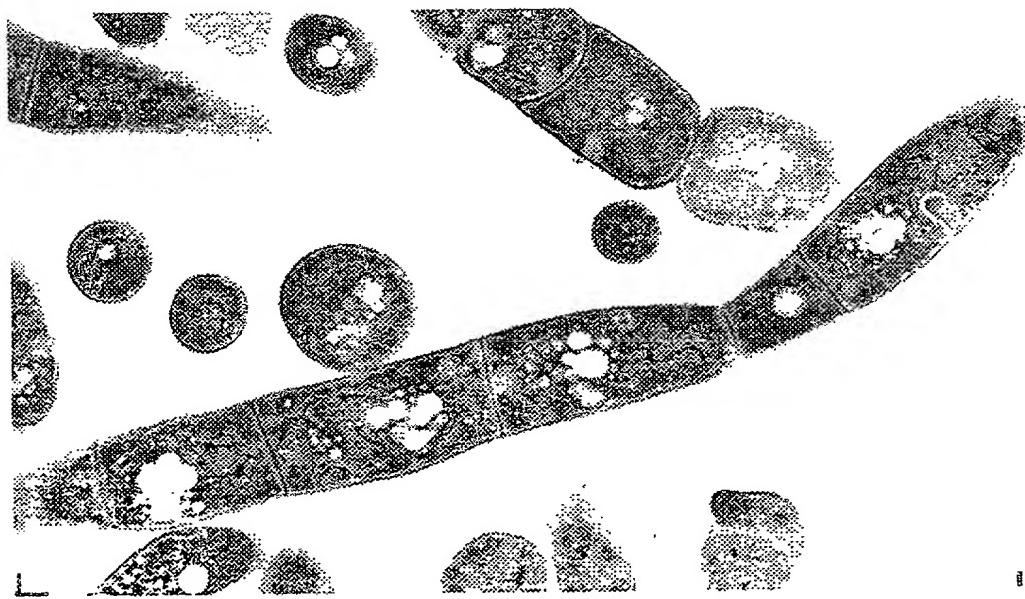
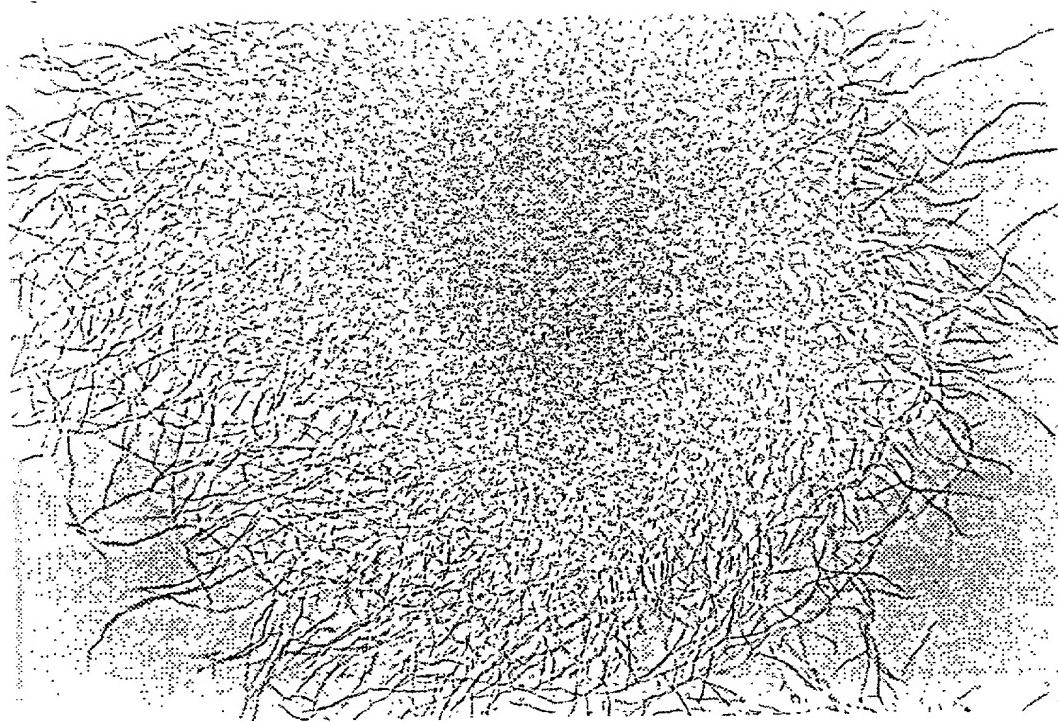
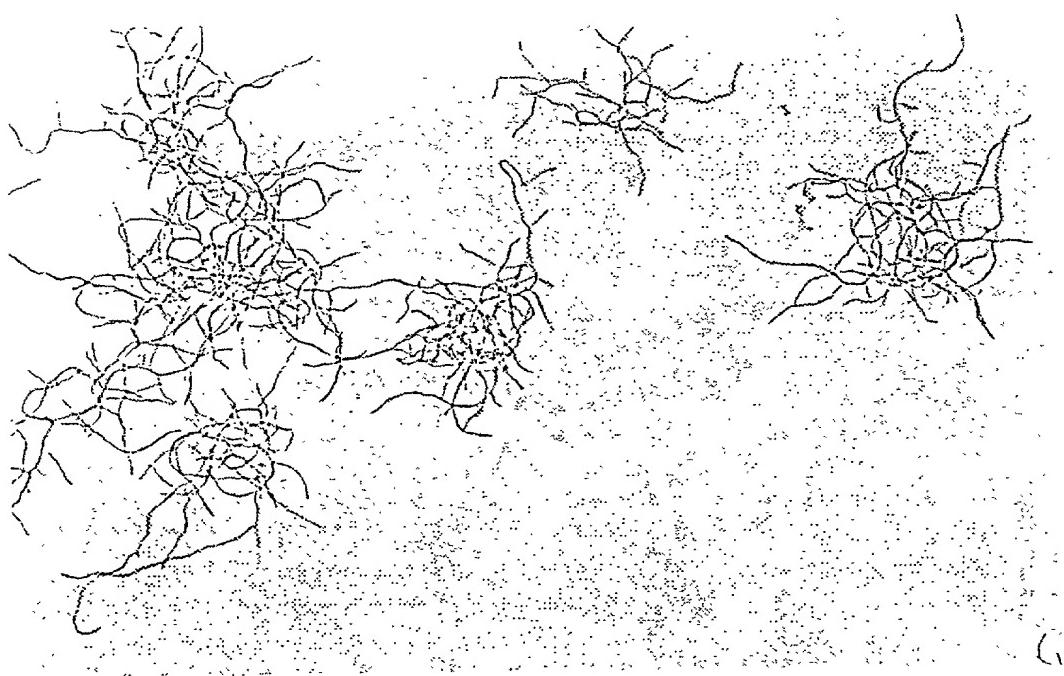


Figure 3C



A



B

Figure 4

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## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

- (A) NAME: Rijksuniversiteit Leiden
- (B) STREET: Stationsweg 46
- (C) CITY: Leiden
- (D) STATE: Zuid-Holland
- (E) COUNTRY: the Netherlands
- (F) POSTAL CODE (ZIP): 2312 AV

- (A) NAME: Nederlandse Organisatie voor Wetenschappelijk Onderzoek/Chemische Wetenschappen/STW
- (B) STREET: Laan van Nieuw Oost Indie 131
- (C) CITY: The Hague
- (D) STATE: Zuid-Holland
- (E) COUNTRY: the Netherlands
- (F) POSTAL CODE (ZIP): 2593 BM

(ii) TITLE OF INVENTION: Reducing branching and enhancing fragmentation in culturing filamentous microorganisms.

(iii) NUMBER OF SEQUENCES: 13

## (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

## (v) CURRENT APPLICATION DATA:

PRIORITY APPLICATION NUMBER : EP 98202148.7

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) Original Source: (A) Organism: Streptomyces griseus  
 (B) Strain: ATCC 23345

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..408
- (D) OTHER INFORMATION: /product= "SsgA"  
     /gene= "ssgA"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATGCGCGAGT CGGTTCAAGC AGAGGTCATG ATGAGCTTCC TCGTCTCCGA GGAGCTCTCG  
 60

TTCCGTATTG CGGTGGAGCT CGGATACGAG GTCGGCGATC CGTATGCCAT CCGGATGACG  
 120

Fig. 5

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TTCCACCTTC CCGGCGATGC CCCTGTGACC TGGGCCTTCG GCGCGGAGCT GCTGCTGGAC  
180

GGGCTCAACA GCCCGAGCGG CGACGGCGAT GTGCACATCG GCGCGACCGA GCGCGAGGGC  
240

CTCGGAGATG TCCACATCCG GCTCCAGGTC GGCGCGGACC GTGCGCTGTT CGGGCGGGG  
300

ACGGCACCGC TGGTGGCGTT CCTCGACCGG ACGGACAAGC TCGTGCCTGCT CGGCCAGGAG  
360

CACACGCTGG GTGACTTCGA CGGCAACCTG GAGGACGCAC TGGGCCCAT CCTCGCCGAG  
420

GAGCAGAACG CGGGCTGA  
438

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptomyces griseus
- (B) STRAIN: ATTC 23345

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..408
- (D) OTHER INFORMATION: /product= "SsgA"  
/gene= "ssgA"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATG AGC TTC CTC GTC TCC GAG GAG CTC TCG TTC CGT ATT CCG GTG GAG  
48

Met Ser Phe Leu Val Ser Glu Glu Leu Ser Phe Arg Ile Pro Val Glu  
1 5 10 15

CTC CGA TAC GAG GTC GGC GAT CCG TAT GCC ATC CGG ATG ACG TTC CAC  
96

Leu Arg Tyr Glu Val Gly Asp Pro Tyr Ala Ile Arg Met Thr Phe His  
20 25 30

CTT CCC GGC GAT GCC CCT GTG ACC TGG GCG TTC GGC CGC GAG CTG CTG  
144

Leu Pro Gly Asp Ala Pro Val Thr Trp Ala Phe Gly Arg Glu Leu Leu  
35 40 45

CTG GAC GGG CTC AAC AGC CCG AGC GGC GAC GGC GAT GTG CAC ATC GGC  
192

Leu Asp Gly Leu Asn Ser Pro Ser Gly Asp Gly Asp Val His Ile Gly  
50 55 60

CCG ACC GAG CCC GAG GGC CTC GGA GAT GTC CAC ATC CGG CTC CAG GTC

Fig. 5 cont.

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240  
 Pro Thr Glu Pro Glu Gly Leu Gly Asp Val His Ile Arg Leu Gln Val  
 65                   70                   75                   80  
 GGC GCG GAC CGT GCG CTG TTC CGG GCG GGG ACG GCA CCG CTG GTG GCG  
 288  
 Gly Ala Asp Arg Ala Leu Phe Arg Ala Gly Thr Ala Pro Leu Val Ala  
 85                   90                   95  
 TTC CTC GAC CGG ACG GAC AAG CTC GTG CCG CTC GGC CAG GAG CAC ACG  
 336  
 Phe Leu Asp Arg Thr Asp Lys Leu Val Pro Leu Gly Gln Glu His Thr  
 100                 105                 110  
 CTG GGT GAC TTC GAC GGC AAC CTG GAG GAC GCA CTG GGC CGC ATC CTC  
 384  
 Leu Gly Asp Phe Asp Gly Asn Leu Glu Asp Ala Leu Gly Arg Ile Leu  
 115                 120                 125  
 GCC GAG GAG CAG AAC GCC GGC TG  
 408  
 Ala Glu Glu Gln Asn Ala Gly  
 130                 135

## (2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met Ser Phe Leu Val Ser Glu Glu Leu Ser Phe Arg Ile Pro Val Glu  
 1                   5                   10                   15  
 Leu Arg Tyr Glu Val Gly Asp Pro Tyr Ala Ile Arg Met Thr Phe His  
 20                 25                   30  
 Leu Pro Gly Asp Ala Pro Val Thr Trp Ala Phe Gly Arg Glu Leu Leu  
 35                 40                   45  
 Leu Asp Gly Leu Asn Ser Pro Ser Gly Asp Gly Asp Val His Ile Gly  
 50                 55                   60  
 Pro Thr Glu Pro Glu Gly Leu Gly Asp Val His Ile Arg Leu Gln Val  
 65                 70                   75                   80  
 Gly Ala Asp Arg Ala Leu Phe Arg Ala Gly Thr Ala Pro Leu Val Ala  
 85                 90                   95  
 Phe Leu Asp Arg Thr Asp Lys Leu Val Pro Leu Gly Gln Glu His Thr  
 100                105                 110  
 Leu Gly Asp Phe Asp Gly Asn Leu Glu Asp Ala Leu Gly Arg Ile Leu  
 115                120                 125  
 Ala Glu Glu Gln Asn Ala Gly  
 130                 135

## (2) INFORMATION FOR SEQ ID NO: 4:

Fig. 5 cont.

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 408 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Streptomyces albus G  
 (B) STRAIN: ATCC 3004

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..408  
 (D) OTHER INFORMATION: /product= "SsgA"  
 /gene= "ssgA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ATG AGC TTC CTC GTC TCC GAG GAG CTC GCC TTC CGC ATC CCG GTG GAG  
 48  
 Met Ser Phe Leu Val Ser Glu Glu Leu Ala Phe Arg Ile Pro Val Glu  
 1 5 10 15

CTG CGG TAC GAG ACC GTC GAT CCG TAC GCG GTG CGG CTG ACG TTC CAC  
 96  
 Leu Arg Tyr Glu Thr Val Asp Pro Tyr Ala Val Arg Leu Thr Phe His  
 20 25 30

CTC CCC GGA GAC GCC CCG GTC ACC TGG GTC TTC GGG CGT GAA CTG CTG  
 144  
 Leu Pro Gly Asp Ala Pro Val Thr Trp Val Phe Gly Arg Glu Leu Leu  
 35 40 45

GTC GAG GGA GTC CTG GAC GCC GCG GGC GAC GGC GAC GTC CGG GTC TGC  
 192  
 Val Glu Gly Val Leu Asp Ala Ala Gly Asp Gly Asp Val Arg Val Cys  
 50 55 60

CCG GTG GGG CAG ACC GCC ACC AGG GAG GTG CAC ATC ACC CTC CAG GTC  
 240  
 Pro Val Gly Gln Thr Ala Thr Arg Glu Val His Ile Thr Leu Gln Val  
 65 70 75 80

GGC TCC GAG CAG GCG CTC TTC CGC GTC GGC AAG GCG CCG CTG CTC GCC  
 288  
 Gly Ser Glu Gln Ala Leu Phe Arg Val Gly Lys Ala Pro Leu Leu Ala  
 85 90 95

TTC CTC GAC CGC ACC GAC CAG GGC TTG TCG CTC GGC AGC GAG CGG GCA  
 336  
 Phe Leu Asp Arg Thr Asp Gln Gly Leu Ser Leu Gly Ser Glu Arg Ala  
 100 105 110

CAC GCC GAC TTC GAC AGC CAC CTC GAC GAC GCT CTG AAC CGC AGC CTC  
 384  
 His Ala Asp Phe Asp Ser His Leu Asp Asp Ala Leu Asn Arg Ser Leu  
 115 120 125

GCC GAG GAG CAG AGC GCC GGC TG  
 408  
 Ala Glu Glu Gln Ser Ala Gly

Fig. 5 cont.

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130

135

## (2) INFORMATION FOR SEQ ID NO: 5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Met	Ser	Phe	Leu	Val	Ser	Glu	Glu	Leu	Ala	Phe	Arg	Ile	Pro	Val	Glu
1				5					10					15	
Leu	Arg	Tyr	Glu	Thr	Val	Asp	Pro	Tyr	Ala	Val	Arg	Leu	Thr	Phe	His
				20				25					30		
Leu	Pro	Gly	Asp	Ala	Pro	Val	Thr	Trp	Val	Phe	Gly	Arg	Glu	Leu	Leu
		35				40					45				
Val	Glu	Gly	Val	Leu	Asp	Ala	Ala	Gly	Asp	Gly	Asp	Val	Arg	Val	Cys
		50			55				60						
Pro	Val	Gly	Gln	Thr	Ala	Thr	Arg	Glu	Val	His	Ile	Thr	Leu	Gln	Val
		65			70			75					80		
Gly	Ser	Glu	Gln	Ala	Leu	Phe	Arg	Val	Gly	Lys	Ala	Pro	Leu	Leu	Ala
		85				90				95					
Phe	Leu	Asp	Arg	Thr	Asp	Gln	Gly	Leu	Ser	Leu	Gly	Ser	Glu	Arg	Ala
		100			105						110				
His	Ala	Asp	Phe	Asp	Ser	His	Leu	Asp	Asp	Ala	Leu	Asn	Arg	Ser	Leu
		115			120					125					
Ala	Glu	Glu	Gln	Ser	Ala	Gly									
		130			135										

## (2) INFORMATION FOR SEQ ID NO: 6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (iii) MOLECULE TYPE: DNA (genomic)

## (vii) HYPOTHETICAL: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptomyces goldiniensis*
- (B) STRAIN: ATCC 21386

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..408
- (D) OTHER INFORMATION: /product= "SsgA"  
/gene= "ssgA"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Fig. 5 cont.

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ATG AGC TTC CTC GTC TCG GAA GAA CTC TCC TTC CGT ATT CCG GTG GAG  
 48  
 Met Ser Phe Leu Val Ser Glu Glu Leu Ser Phe Arg Ile Pro Val Glu  
 1 5 10 15

CTG CGT TAC GAG ACC TGT GAT CCC TAC GCC GTG CGG CTG ACC TTT CAT  
 96  
 Leu Arg Tyr Glu Thr Cys Asp Pro Tyr Ala Val Arg Leu Thr Phe His  
 20 25 30

CTG CCC GGA GAT GCC CCG GTG ACC TGG GCG TTC GGG CGG GAG TTG CTC  
 144  
 Leu Pro Gly Asp Ala Pro Val Thr Trp Ala Phe Gly Arg Glu Leu Leu  
 35 40 45

ATC GAC GGA GGT CCG CGG CCG TGC GGG GAC GGG GAC GTC CAC ATC GCG  
 192  
 Ile Asp Gly Pro Arg Pro Cys Gly Asp Gly Asp Val His Ile Ala  
 50 55 60

CCC GCC GAC CCG GAG ACG TTC GGC GAG GTC CTG ATC CGC CTG CAG GTG  
 240  
 Pro Ala Asp Pro Glu Thr Phe Gly Glu Val Leu Ile Arg Leu Gln Val  
 65 70 75 80

GGG AGC GAC CAG GCG ATG TTC CGG GTC GGC ACG GCG CCG CTG GTG GCC  
 288  
 Gly Ser Asp Gln Ala Met Phe Arg Val Gly Thr Ala Pro Leu Val Ala  
 85 90 95

TTC CTG GAC CGC ACG GAC AAG ATC GTG CCG CTG GGG CAG GAG CGT TCC  
 336  
 Phe Leu Asp Arg Thr Asp Lys Ile Val Pro Leu Gly Gln Glu Arg Ser  
 100 105 110

CTC GCC GAC TTC GAC GCC CTG CTC GAC GAG GCG CTG GAC CGC ATC CTG  
 384  
 Leu Ala Asp Phe Asp Ala Leu Leu Asp Glu Ala Leu Asp Arg Ile Leu  
 115 120 125

GCC GAG GAG CAG AAC GCC GGC TG  
 408  
 Ala Glu Glu Gln Asn Ala Gly  
 130 135

## (2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met Ser Phe Leu Val Ser Glu Glu Leu Ser Phe Arg Ile Pro Val Glu  
 1 5 10 15

Leu Arg Tyr Glu Thr Cys Asp Pro Tyr Ala Val Arg Leu Thr Phe His  
 20 25 30

Leu Pro Gly Asp Ala Pro Val Thr Trp Ala Phe Gly Arg Glu Leu Leu  
 35 40 45

Fig. 5 cont.

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Ile Asp Gly Gly Pro Arg Pro Cys Gly Asp Gly Asp Val His Ile Ala  
 50 55 60

Pro Ala Asp Pro Glu Thr Phe Gly Glu Val Leu Ile Arg Leu Gln Val  
 65 70 75 80

Gly Ser Asp Gln Ala Met Phe Arg Val Gly Thr Ala Pro Leu Val Ala  
 85 90 95

Phe Leu Asp Arg Thr Asp Lys Ile Val Pro Leu Gly Gln Glu Arg Ser  
 100 105 110

Leu Ala Asp Phe Asp Ala Leu Leu Asp Glu Ala Leu Asp Arg Ile Leu  
 115 120 125

Ala Glu Glu Gln Asn Ala Gly  
 130 135

## (2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 408 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Streptomyces netropsis
  - (B) STRAIN: ATCC 23940
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..408
  - (D) OTHER INFORMATION: /product= "SsgA"  
/gene= "ssgA"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

ATG AGC TTC CTC GTC TCC GAG GAG CTC TCC TTC AAG ATC CCA GTC GAA  
 48

Met Ser Phe Leu Val Ser Glu Glu Leu Ser Phe Lys Ile Pro Val Glu  
 1 5 10 15

CTG CGA TAC GAG ACC CGG GAT CCC TAC GCG GTG CGG ATG ACC TTC CAC  
 96

Leu Arg Tyr Glu Thr Arg Asp Pro Tyr Ala Val Arg Met Thr Phe His  
 20 25 30

CTC CCC GGA GAC GCG CCT GTG ACC TGG GCG TTC GCC CGG GAG CTG CTG  
 144

Leu Pro Gly Asp Ala Pro Val Thr Trp Ala Phe Gly Arg Glu Leu Leu  
 35 40 45

CTC GAC GGG ATC AAC CGC CCG AGC GGC GAC GGC GAC GTC CAC ATC GCC  
 192

Leu Asp Gly Ile Asn Arg Pro Ser Gly Asp Gly Asp Val His Ile Ala  
 50 55 60

CCG ACC GAC CCC GAG GGC CTG TCG GAC GTC TCC ATC CGG CTC CAG GTG

Fig. 5 cont.

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240  
 Pro Thr Asp Pro Glu Gly Leu Ser Asp Val Ser Ile Arg Leu Gln Val  
 65 70 75 80

GGC GCG GAC CGC GCC CTC TTC CGT GCA GGC GCC CCG CCG CTG GTC GCC  
 288  
 Gly Ala Asp Arg Ala Leu Phe Arg Ala Gly Ala Pro Pro Leu Val Ala  
 85 90 95

TTC CTC GAC CGC ACG GAC AAG TCG GTG CCG CTC GGT CAG GAA CAG ACT  
 336  
 Phe Leu Asp Arg Thr Asp Lys Ser Val Pro Leu Gly Gln Glu Gln Thr  
 100 105 110

CTG GGT GAC TTC GAG GAC AGC CTG GAG GCC GCG CTC GGC AAG ATC CTC  
 384  
 Leu Gly Asp Phe Glu Asp Ser Leu Glu Ala Ala Leu Gly Lys Ile Leu  
 115 120 125

GCC GAG GAG CAG AAC GCC GGC TG  
 408  
 Ala Glu Glu Gln Asn Ala Gly  
 130 135

## (2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 135 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Met Ser Phe Leu Val Ser Glu Glu Leu Ser Phe Lys Ile Pro Val Glu  
 1 5 10 15

Leu Arg Tyr Glu Thr Arg Asp Pro Tyr Ala Val Arg Met Thr Phe His  
 20 25 30

Leu Pro Gly Asp Ala Pro Val Thr Trp Ala Phe Gly Arg Glu Leu Leu  
 35 40 45

Leu Asp Gly Ile Asn Arg Pro Ser Gly Asp Gly Asp Val His Ile Ala  
 50 55 60

Pro Thr Asp Pro Glu GLy Leu Ser Asp Val Ser Ile Arg Leu Gln Val  
 65 70 75 80

Gly Ala Asp Arg Ala Leu Phe Arg Ala Gly Ala Pro Pro Leu Val Ala  
 85 90 95

Phe Leu Asp Arg Thr Asp Lys Ser Val Pro Leu Gly Gln Glu Gln Thr  
 100 105 110

Leu Gly Asp Phe Glu Asp Ser Leu Glu Ala Ala Leu Gly Lys Ile Leu  
 115 120 125

Ala Glu Glu Gln Asn Ala Gly  
 130 135

## (2) INFORMATION FOR SEQ ID NO: 10:

Fig. 5 cont.

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 nucleotides
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (synthetic)
- (vi) ORIGINAL SOURCE:
  - (C) INDIVIDUAL PRODUCT: ssg1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
 GGCGAATTCTG AACAGCTACG TGGCGAAGTC GCCA  
 34

## (2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 nucleotides
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (synthetic)
- (vi) ORIGINAL SOURCE:
  - (C) INDIVIDUAL PRODUCT: ssg2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
 GTGGGATCCG TGCTCGCGGC GCTGGTCGTC TC  
 32

## (2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 nucleotides
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (synthetic)
- (vi) ORIGINAL SOURCE:
  - (C) INDIVIDUAL PRODUCT: ssg3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
 GGGAAATTCCA TATGCGCGAG TCGGTTCAAG CA  
 32

## (2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 nucleotides
  - (B) TYPE: nucleic acid

Fig. 5 cont.

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(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL PRODUCT: ssg4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CCGGTCAGCC GGC GTT CTG C TCCTC  
25

Fig. 5 cont.